

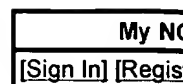
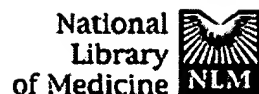
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DNA-methyltransferases of *Yersinia pestis* EV, plague agent bacteria were isolated by P-II phosphocellulose chromatography. The methylating activity is eluted by two fractions at the 0.47 M and 0.53 M NaCl concentrations. Methylases of the plague microbe are specific with respect to two bases (adenine and cytosine) and are capable of modifying both native and denaturated form of DNA.

PMID: 6636308 [PubMed - indexed for MEDLINE]

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[Comparison of specific recognition sites of adenine and cytosine DNA-methylase of Yersinia

Pestis EV 76 C dam and dcm by Escherichia coli methylases]

Biokhimiia. 1984 Oct;49(10):1594-7. Russian.

PMID: 6097301 [PubMed - indexed for MEDLINE]

Gene. 1994 Mar 11;140(1):67-71.

Related Articles, Links

The DNA adenine methyltransferase-encoding gene (dam) of *Vibrio cholerae*.

Bandyopadhyay R, Das J.

Biophysics Division, Indian Institute of Chemical Biology, Calcutta.

The DNA adenine methyltransferase (MTase)-encoding gene (dam) of *Vibrio cholerae*, an organism belonging to the family Vibrionaceae, has been cloned and the complete nucleotide (nt) sequence determined. *V. cholerae* dam encodes a 21.5-kDa protein and is directly involved in methyl-directed DNA mismatch repair. It can substitute for the *Escherichia coli* enzyme and can suppress the phenotypic traits associated with *E. coli* dam mutants. Overproduction of *V. cholerae* Dam MTase does not result in hypermutability in either *V. cholerae* or *E. coli* cells.

Overproduction of *V. cholerae* Dam in a pUC plasmid, however, fails to suppress the 2-aminopurine (2-AP)-sensitive phenotype of *E. coli* dam mutants. Homology between the nt and deduced amino acid (aa) sequences of the *E. coli* and *V. cholerae* dam genes is only 30-35%.

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MTB3_BACAR	(P22772),	MTBB_BACSU	(P33563),	MTC1_BACST	(P43423),
MTC1_CAUCR	(Q45971),	MTC1_PBCVC	(Q01511),	MTC2_PBCV1	(P31118),
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MTF1_FLAOK	(P14871),	MTH1_HAEIN	(P20590),	MTH1_HAEPa	(P29538),
MTH2_HAEHA	(P00473),	MTH3_HAEIN	(P43871),	MTHB_HAEPH	(P50193),
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T1MP_ECOLI	(Q47163),	T1M_SALPO	(P07989),	T1M_SALTY	(P40813),
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Y1368_XYLFA ([Q9PDL1](#)), Y1655_NEIMB ([Q9JYC0](#)), Y1678_PSEAE ([Q9I347](#)),
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Y2118_VIBCH ([Q9KQ83](#)), Y3402_METJA ([Q60301](#)), Y390_PASMU ([Q9CNN7](#)),
Y606_XYLFT ([Q87DS5](#)), YFCB_ECOLI ([P39199](#)), YFCB_SALTI ([P0A294](#)),
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DMA_BPT2 (P12427)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (M.EcoT2Dam).
{GENE: Name=DAM} - Bacteriophage T2

DMA_BPT4 (P04392)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (M.EcoT4Dam).
{GENE: Name=DAM} - Bacteriophage T4

DMA_ECOLI (P00475)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.EcoDam). {GENE: Name=dam; OrderedLocusNames=b3387, z4740, ECs4229} - Escherichia coli, Escherichia coli O157:H7

DMA_HAEIN (P44431)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.HindIV). {GENE: Name=dam; Synonyms=hindIVM; OrderedLocusNames=HI0209} - Haemophilus influenzae

DMA_SALTI (P0A292)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.StyDam). {GENE: Name=dam; OrderedLocusNames=STY4312, t4022} - Salmonella typhi

DMA_SALTY (P0A291)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.StyDam). {GENE: Name=dam; OrderedLocusNames=STM3484} - Salmonella typhimurium

DMA_SERMA (P45454)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.SmaII). {GENE: Name=dam} - Serratia marcescens

DMA_TREPA (O33844)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.TpaI). {GENE: Name=dam; OrderedLocusNames=TP0810} - *Treponema pallidum*

DMA_VIBCH (Q08318)

DNA adenine methylase (EC 2.1.1.72) (Deoxyadenosyl-methyltransferase) (DNA adenine methyltransferase) (M.VchADam). {GENE: Name=dam; OrderedLocusNames=VC2626} - *Vibrio cholerae*

MTM2_MORBO (P23192)

Modification methylase MboII (EC 2.1.1.72) (Adenine-specific methyltransferase MboII) (M.MboII) (DNA MTase MboIIA). {GENE: Name=mboIIM} - *Moraxella bovis*

□ 1: Biochem Biophys Res Commun. 1989 Dec 15;165(2):561-7.

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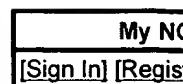
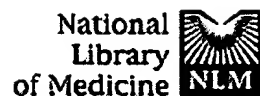
A mutation in the dam gene of *Vibrio cholerae*: 2-aminopurine sensitivity with intact GATC methylase activity.

Bandyopadhyay R, Sengupta A, Das J.

Biophysics Division, Indian Institute of Chemical Biology, Calcutta.

Vibrio cholerae mutants sensitive to 2-aminopurine (2AP) but with DNA adenine methylase activity similar to parental cells have been isolated. The mutant strains were sensitive to ultraviolet light (UV), methyl methane sulphonate (MMS) and 9-aminoacridine. The spontaneous mutation frequency of the mutants were not significantly affected. Attempts to isolate *dam* *V. cholerae* cells by screening 2AP sensitive cells have not been successful. All the mutant phenotypes could be suppressed by introducing the plasmid pRB103 carrying the *dam* gene of *Escherichia coli* into the mutant cells.

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[Comparison of specific recognition sites of adenine and cytosine DNA-methylase of Yersinia Pestis EV 76 C dam and dcm by Escherichia coli methylases]

[Article in Russian]

Demidova GV, Goncharov EK, Tynianova VI.

Using enzymatic modelling of in vitro methylation of chromosome DNAs from Yersinia pestis EV 76, E. coli 834 and E. coli C600 RII by DNA methylases of Eco RII and Eco dam as well as of DNA hydrolysis of plasmid pBR 322 from the cells of Y. pestis EV 76, E. coli C600 and E. coli 834 by restrictases of Eco RII and Cfu I, it was found that cytosine DNA methylase from plague bacteria does not correspond to the type of RII methylases of E. coli. Adenyl DNA methylase is related to E. coli methylases type dam and modifies adenine in the nucleotide sequence of GATC.

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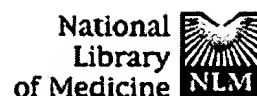
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☐ 2. 20050131222. 05 Nov 04. 16 Jun 05. Nucleotide sequence of the *haemophilus influenzae* Rd genome, fragments thereof, and uses thereof. Fleischmann, Robert D., et al. 536/23.7; C07H021/04.

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- ☐ 16. 6846651. 03 Jun 02; 25 Jan 05. Nucleotide sequence of the *Haemophilus influenzae* Rd genome, fragments thereof, and uses thereof. Fleischmann; Robert D., et al. 435/69.1; 435/252.3 435/320.1 536/23.7. C12N015/63 C12N001/21 C12N015/31.
- ☐ 17. 6528289. 23 Aug 00; 04 Mar 03. Nucleotide sequence of the *Haemophilus influenzae* Rd genome, fragments thereof, and uses thereof. Fleischmann; Robert D., et al. 435/91.41; 435/252.3 435/320.1 435/6 536/23.1 536/23.7. C12N015/64.
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- ☐ 20. 6468765. 07 Jun 95; 22 Oct 02. Selected *Haemophilus influenzae* Rd polynucleotides and polypeptides. Fleischmann; Robert D., et al. 435/69.1; 435/252.3 435/320.1 435/6 536/23.1 536/23.7 536/24.32. G12P021/02.
- ☐ 21. 6355450. 07 Jun 95; 12 Mar 02. Computer readable genomic sequence of *Haemophilus influenzae* Rd, fragments thereof, and uses thereof. Fleischmann; Robert D., et al. 435/69.1; 435/252.3 435/320.1 435/851 536/23.1 536/23.7 536/24.32 536/24.33. C12P021/06 C12N001/20 C12N015/00 C07H021/04.
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- ☐ 23. US20020077272A. Reducing bacterial virulence using an agent that alters the bacteria's native level of DNA methyltransferase activity. HEITHOFF, D M, et al. A61K031/00 A61K031/52.

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TITLE: Host cells deficient for mismatch repair and their use in methods for inducing homologous recombination using single-stranded nucleic acids

PUBLICATION-DATE: April 14, 2005

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ABSTRACT:

Methods are disclosed herein for inducing homologous recombination

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